CRF ~~Error or~~ Corrected by the STIC Syst〇 Branch

Serial Number: 10/066,127

CRF Processing Date: 5/30/2002
Edited by: _____
Verified by: _____ (STIC staff)

OIPE 0590
2977

ENTERED

☐ Changed a file from non-ASCII to ASCII.

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95
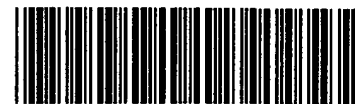
OIPE

RAW SEQUENCE LISTING   DATE: 05/30/2002
PATENT APPLICATION: US/10/066,127   TIME: 07:53:08

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\05302002\J066127.raw

```
   3 <110> APPLICANT: HYBRIGENICS
   4       Pierre, LEGRAIN
   6 <120> TITLE OF INVENTION: Identification of the Anti-s28 Factor in Helicobacter
pylori, in
   7       Campylobacter jejuni and in Pseudomonas aeruginosa and Application Thereof
   9 <130> FILE REFERENCE: B4797A
  11 <140> CURRENT APPLICATION NUMBER: US 10/066,127
  12 <141> CURRENT FILING DATE: 2002-01-31
  14 <150> PRIOR APPLICATION NUMBER: US 60/265,465
  15 <151> PRIOR FILING DATE: 2001-01-31
  17 <160> NUMBER OF SEQ ID NOS: 29
  19 <170> SOFTWARE: PatentIn version 3.1
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 90
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Helicobacter pylori
  26 <220> FEATURE:
W--> 27 <221> NAME/KEY: SID1122
  28 <222> LOCATION: (1)..(90)
  29 <223> OTHER INFORMATION: the Selected Interacting Domain (SID(r)) of HP1122
  32 <400> SEQUENCE: 1
  33 atcaagaaag cgattgaaaa taaccagtat aaaatcaact tgcatgagac ttctcacaaa      60
  35 atggcaaagg atttattggg gataagctag                                      90
  38 <210> SEQ ID NO: 2
  39 <211> LENGTH: 29
  40 <212> TYPE: PRT
  41 <213> ORGANISM: Helicobacter pylori
  43 <220> FEATURE:
W--> 44 <221> NAME/KEY: SID1122
  45 <222> LOCATION: (1)..(29)
  46 <223> OTHER INFORMATION:
  49 <400> SEQUENCE: 2
  51 Ile Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu
  52 1               5                   10                  15
  55 Thr Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
  56             20                  25
  59 <210> SEQ ID NO: 3
  60 <211> LENGTH: 177
  61 <212> TYPE: DNA
  62 <213> ORGANISM: Helicobacter pylori
  64 <220> FEATURE:
W--> 65 <221> NAME/KEY: SID1032
  66 <222> LOCATION: (1)..(177)
  67 <223> OTHER INFORMATION: the Selected Interacting Domain (SID(r)) HP1032
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Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\05302002\J066127.raw**

```
 70 <400> SEQUENCE: 3
 71 aaagcgctga atcaaatgag cgaaagagag caaatcctta tccagcttta ttactttgaa      60
 73 gagttgaatt tgagcgagat taaagagatt ttaggcatta ctgaatcgcg catttctcaa     120
 75 atcattaaag aagtgattaa aaaggtgcgt aaatccttag gagtggatca tggctga        177
 78 <210> SEQ ID NO: 4
 79 <211> LENGTH: 58
 80 <212> TYPE: PRT
 81 <213> ORGANISM: Helicobacter pylori
 83 <220> FEATURE:
W--> 84 <221> NAME/KEY: SID1032
 85 <222> LOCATION: (1)..(58)
 86 <223> OTHER INFORMATION:
 89 <400> SEQUENCE: 4
 91 Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu Ile Gln Leu
 92 1               5                   10                  15
 95 Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu Ile Leu Gly
 96             20                  25                  30
 99 Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val Ile Lys Lys
100         35                  40                  45
103 Val Arg Lys Ser Leu Gly Val Asp His Gly
104     50                  55
107 <210> SEQ ID NO: 5
108 <211> LENGTH: 231
109 <212> TYPE: DNA
110 <213> ORGANISM: Helicobacter pylori
112 <220> FEATURE:
W--> 113 <221> NAME/KEY: HP1122
114 <222> LOCATION: (1)..(231)
115 <223> OTHER INFORMATION: the ORF of sigma28 factor
118 <400> SEQUENCE: 5
119 atgaatatca aattaaagga ttttacaatg attaatgccg tttcttctct tgctccggtg      60
121 cagtctttgg ggaattataa gcgtgtggaa aagaatgaaa aagttgaaaa caatgaggcc     120
123 gctcttgata gggtagctga gatcaagaaa gcgattgaaa ataaccagta taaaatcaac     180
125 ttgcatgaga cttctcacaa aatggcaaag gatttattgg ggataagcta g             231
128 <210> SEQ ID NO: 6
129 <211> LENGTH: 76
130 <212> TYPE: PRT
131 <213> ORGANISM: Helicobacter pylori
133 <220> FEATURE:
W--> 134 <221> NAME/KEY: HP1122
135 <222> LOCATION: (1)..(76)
136 <223> OTHER INFORMATION:
139 <400> SEQUENCE: 6
141 Met Asn Ile Lys Leu Lys Asp Phe Thr Met Ile Asn Ala Val Ser Ser
142 1               5                   10                  15
145 Leu Ala Pro Val Gln Ser Leu Gly Asn Tyr Lys Arg Val Glu Lys Asn
146             20                  25                  30
149 Glu Lys Val Glu Asn Asn Glu Ala Ala Leu Asp Arg Val Ala Glu Ile
150         35                  40                  45
```

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Input Set : A:\PTO.AMC.txt
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```
153 Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
154     50              55              60
157 Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
158 65              70              75
161 <210> SEQ ID NO: 7
162 <211> LENGTH: 768
163 <212> TYPE: DNA
164 <213> ORGANISM: Helicobacter pylori
166 <220> FEATURE:
```
W--> 167 `<221> NAME/KEY: HP1032`
```
168 <222> LOCATION: (1)..(768)
169 <223> OTHER INFORMATION: The ORF of anti sigma 28 factor
172 <400> SEQUENCE: 7
173 atgattttga tgatggaaaa tagaatgccc aaaggaattc aaaaaactga aacaagcgaa      60
175 aaaaatatag aaaaggtttt gaacgcctat gataagcaac aacaccacca tcaagacgat     120
177 ctcgctattc agtatttacc agccgtgcgc gccatggcgt ttcgtctaaa agagcgcttg     180
179 cccagctcta ttgattttaa cgatctggtt tctattggca ctgaagaatt gattaaatta     240
181 gccaggcgtt atgagagcgc gttaaacgat tctttttggg ggtatgcgaa gactcgtgtc     300
183 aatggggcga tgttagatta tttgcgctct ttagatgtga tttctcgctc tagcaggaaa     360
185 ctcattaaaa gcattgatat tgaaatcacc aaacacctta tgagcatgg gaaagagcct     420
187 agcgatgcgt atttagcgca aactttaggc gaaaatattg aaaaaattaa agaagccaaa     480
189 acggcttcag atatttatgc gttagtgcca atagatgaac aattcaatgc gattgagcaa     540
191 gatgaaatca ctaaaaaaat tgaagcagaa gagttgttag agcatgtcca aaaagcgctg     600
193 aatcaaatga gcgaaagaga gcaaatcctt atccagcttt attactttga gagttgaat     660
195 ttgagcgaga ttaaagagat tttaggcatt actgaatcgc gcatttctca aatcattaaa     720
197 gaagtgatta aaaaggtgcg taaatcctta ggagtggatc atggctga                 768
200 <210> SEQ ID NO: 8
201 <211> LENGTH: 255
202 <212> TYPE: PRT
203 <213> ORGANISM: Helicobacter pylori
205 <220> FEATURE:
```
W--> 206 `<221> NAME/KEY: HP1032`
```
207 <222> LOCATION: (1)..(255)
208 <223> OTHER INFORMATION:
211 <400> SEQUENCE: 8
213 Met Ile Leu Met Met Glu Asn Arg Met Pro Lys Gly Ile Gln Lys Thr
214 1               5               10              15
217 Glu Thr Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys
218             20              25              30
221 Gln Gln His His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala
222         35              40              45
225 Val Arg Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile
226     50              55              60
229 Asp Phe Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu
230 65              70              75              80
233 Ala Arg Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala
234             85              90              95
237 Lys Thr Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp
238             100             105             110
```

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```
241 Val Ile Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu
242         115                 120                 125
245 Ile Thr Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr
246         130                 135                 140
249 Leu Ala Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys
250 145             150                 155                 160
253 Thr Ala Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn
254             165                 170                 175
257 Ala Ile Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu
258             180                 185                 190
261 Leu Glu His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln
262         195                 200                 205
265 Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile
266         210                 215                 220
269 Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys
270 225                 230                 235                 240
273 Glu Val Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
274             245                 250                 255
277 <210> SEQ ID NO: 9
278 <211> LENGTH: 65
279 <212> TYPE: PRT
280 <213> ORGANISM: Campylobacter jejuni
282 <220> FEATURE:
```
W--> `283 <221> NAME/KEY: Cj1464`
```
284 <222> LOCATION: (1)..(65)
285 <223> OTHER INFORMATION: Cj1464 protein
288 <400> SEQUENCE: 9
290 Met Ile Asn Pro Ile Gln Gln Ser Tyr Val Ala Asn Thr Ala Leu Asn
291 1               5                   10                  15
294 Thr Asn Arg Ile Asp Lys Glu Thr Lys Thr Asn Asp Thr Gln Lys Thr
295             20                  25                  30
298 Glu Asn Asp Lys Ala Ser Lys Ile Ala Glu Gln Ile Lys Asn Gly Thr
299         35                  40                  45
302 Tyr Lys Ile Asp Thr Lys Ala Thr Ala Ala Ala Ile Ala Asp Ser Leu
303     50                  55                  60
306 Ile
307 65
310 <210> SEQ ID NO: 10
311 <211> LENGTH: 107
312 <212> TYPE: PRT
313 <213> ORGANISM: Pseudomonas aeruginosa
315 <220> FEATURE:
```
W--> `316 <221> NAME/KEY: PA3351`
```
317 <222> LOCATION: (1)..(107)
318 <223> OTHER INFORMATION: PA3351 protein
321 <400> SEQUENCE: 10
323 Met Val Ile Asp Phe Asn Arg Leu Asn Pro Gly Ser Thr Pro Ala Thr
324 1               5                   10                  15
327 Thr Gly Arg Thr Gly Ser Thr Ala Ala Gly Arg Pro Asp Ala Thr Gly
```

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Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\05302002\J066127.raw**

```
328            20                  25                  30
331 Ala Asp Lys Ala Gly Gln Ala Ala Thr Ser Ala Pro Lys Ser Gly Glu
332         35                  40                  45
335 Ser Val Gln Ile Ser Glu Thr Ala Gln Asn Met Gln Lys Val Thr Asp
336     50                  55                  60
339 Gln Leu Gln Thr Leu Pro Val Val Asp Asn Asp Lys Val Ala Arg Ile
340 65                  70                  75                  80
343 Lys Gln Ala Ile Ala Asp Gly Thr Tyr Gln Val Asp Ser Glu Arg Val
344             85                  90                  95
347 Ala Ser Lys Leu Leu Asp Phe Glu Ser Gln Arg
348         100                 105
351 <210> SEQ ID NO: 11
352 <211> LENGTH: 32
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: primer PCR 1550
359 <400> SEQUENCE: 11
360 catgagatct ctataaaaac agagcggcta aa                           32
363 <210> SEQ ID NO: 12
364 <211> LENGTH: 42
365 <212> TYPE: DNA
366 <213> ORGANISM: Artificial sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: primer PCR 1551
371 <400> SEQUENCE: 12
372 tgacgcatgc actagtcata tgatgttcct tgttttttga tg                42
375 <210> SEQ ID NO: 13
376 <211> LENGTH: 42
377 <212> TYPE: DNA
378 <213> ORGANISM: artificial sequence
380 <220> FEATURE:
381 <223> OTHER INFORMATION: linker
383 <400> SEQUENCE: 13
384 tgacgcatgc actagtcata tgatgttcct tgttttttga tg                42
387 <210> SEQ ID NO: 14
388 <211> LENGTH: 22
389 <212> TYPE: DNA
390 <213> ORGANISM: artificial sequence
392 <220> FEATURE:
393 <223> OTHER INFORMATION: primer PCR 2386
395 <400> SEQUENCE: 14
396 gctcggtacc cgggtgacta ac                                      22
399 <210> SEQ ID NO: 15
400 <211> LENGTH: 27
401 <212> TYPE: DNA
402 <213> ORGANISM: artificial sequence
404 <220> FEATURE:
405 <223> OTHER INFORMATION: primer PCR 2387
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/066,127

DATE: 05/30/2002
TIME: 07:53:09

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\05302002\J066127.raw**

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L:27  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:44  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:65  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:84  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:113 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:134 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
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